

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/637,302

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
Indicate in the (ix) feature section that some may be missing.
- 7 ☒ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) 7. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) _____ are missing this mandatory field or its response.
- 12 ☒ Use of <220>Feature (NEW RULES) Sequence(s) #7 are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING DATE: 08/23/2000
 PATENT APPLICATION: US/09/637,302 TIME: 09:32:54

Input Set : A:\TSR7102.txt
 Output Set: N:\CRF3\08232000\I637302.raw

3 <110> APPLICANT: HOOD, John
 4 ELICEIRI, Brian
 5 CHERESH, David
 7 <120> TITLE OF INVENTION: Methods and Compositions Useful for Modulation of
 8 Angiogenesis Using Tyrosine Kinase Raf and Ras
 10 <130> FILE REFERENCE: TSRI 710.2
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/637,302
 C--> 13 <141> CURRENT FILING DATE: 2000-08-11
 15 <150> PRIOR APPLICATION NUMBER: US 60/148,924
 16 <151> PRIOR FILING DATE: 1999-08-13
 18 <150> PRIOR APPLICATION NUMBER: US 60/215,951
 19 <151> PRIOR FILING DATE: 2000-07-05
 21 <160> NUMBER OF SEQ ID NOS: 7
 23 <170> SOFTWARE: PatentIn Ver. 2.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 2977
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Homo sapiens
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS /
 32 <222> LOCATION: (130)..(2073)
 34 <400> SEQUENCE: 1
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 37 tgccgcccgaac cgacaggacg ttggggcggc ctggctccct caggtttaag aattgttta 120
 39 gctgcatca atg gag cac ata cag gga gct tgg aag acg atc agc aat ggt 171
 40 Met Glu His Ile Gln Gly Ala Trp Lys Thr Ile Ser Asn Gly
 41 1 5 10
 43 ttt gga ttc aaa gat gcc gtg ttt gat ggc tcc agc tgc atc tct cct 219
 44 Phe Gly Phe Lys Asp Ala Val Phe Asp Gly Ser Ser Cys Ile Ser Pro
 45 15 20 25 30
 47 aca ata gtt cag cag ttt ggc tat cag cgc cgg gca tca gat gat ggc 267
 48 Thr Ile Val Gln Gln Phe Gly Tyr Gln Arg Arg Ala Ser Asp Asp Gly
 49 35 40 45
 51 aaa ctc aca gat cct tct aag aca agc aac act atc cgt gtt ttc ttg 315
 52 Lys Leu Thr Asp Pro Ser Lys Thr Ser Asn Thr Ile Arg Val Phe Leu
 53 50 55 60
 55 ccg aac aag caa aga aca gtg gtc aat gtg cga aat gga atg agc ttg 363
 56 Pro Asn Lys Gln Arg Thr Val Val Asn Val Arg Asn Gly Met Ser Leu
 57 65 70 75
 59 cat gac tgc ctt atg aaa gca ctc aag gtg agg ggc ctg caa cca gag 411
 60 His Asp Cys Leu Met Lys Ala Leu Lys Val Arg Gly Leu Gln Pro Glu
 61 80 85 90
 63 tgc tgt gca gtg ttc aga ctt ctc cac gaa cac aaa ggt aaa aaa gca 459
 64 Cys Cys Ala Val Phe Arg Leu Leu His Glu His Lys Gly Lys Lys Ala
 65 95 100 105 110
 67 cgc tta gat tgg aat act gat gct gcg tct ttg att gga gaa gaa ctt 507
 68 Arg Leu Asp Trp Asn Thr Asp Ala Ala Ser Leu Ile Gly Glu Glu Leu

see p. 6
 Does Not Comply
 Corrected Diskette Needed

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/637,302

DATE: 08/23/2000
 TIME: 09:32:54

Input Set : A:\TSR7102.txt
 Output Set : N:\CRF3\08232000\I637302.raw

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71  caa gta gat ttc ctg gat cat gtt ccc ctc aca aca cac aac ttt gct 555
72  Gln Val Asp Phe Leu Asp His Val Pro Leu Thr Thr His Asn Phe Ala
73          130          135          140
75  cgg aag acg ttc ctg aag ctt gcc ttc tgt gac atc tgt cag aaa ttc 603
76  Arg Lys Thr Phe Leu Lys Leu Ala Phe Cys Asp Ile Cys Gln Lys Phe
77          145          150          155
79  ctg ctc aat gga ttt cga tgt cag act tgt ggc tac aaa ttt cat gag 651
80  Leu Leu Asn Gly Phe Arg Cys Gln Thr Cys Gly Tyr Lys Phe His Glu
81          160          165          170
83  cac tgt agc acc aaa gta cct act atg tgt gtg gac tgg agt aac atc 699
84  His Cys Ser Thr Lys Val Pro Thr Met Cys Val Asp Trp Ser Asn Ile
85          175          180          185          190
87  aga caa ctc tta ttg ttt cca aat tcc act att ggt gat agt gga gtc 747
88  Arg Gln Leu Leu Phe Pro Asn Ser Thr Ile Gly Asp Ser Gly Val
89          195          200          205
91  cca gca cta cct tct ttg act atg cgt cgt atg cga gag tct gtt tcc 795
92  Pro Ala Leu Pro Ser Leu Thr Met Arg Arg Met Arg Glu Ser Val Ser
93          210          215          220
95  agg atg cct gtt agt tct cag cac aga tat tct aca cct cac gcc ttc 843
96  Arg Met Pro Val Ser Ser Gln His Arg Tyr Ser Thr Pro His Ala Phe
97          225          230          235
99  acc ttt aac acc tcc agt ccc tca tct gaa ggt tcc ctc tcc cag agg 891
100  Thr Phe Asn Thr Ser Ser Pro Ser Ser Glu Gly Ser Leu Ser Gln Arg
101          240          245          250
103  cag agg tcg aca tcc aca cct aat gtc cac atg gtc agc acc acg ctg 939
104  Gln Arg Ser Thr Ser Thr Pro Asn Val His Met Val Ser Thr Thr Leu
105          255          260          265          270
107  cct gtg gac agc agg atg att gag gat gca att cga agt cac agc gaa 987
108  Pro Val Asp Ser Arg Met Ile Glu Asp Ala Ile Arg Ser His Ser Glu
109          275          280          285
111  tca gcc tca cct tca gcc ctg tcc agt agc ccc aac aat ctg agc cca 1035
112  Ser Ala Ser Pro Ser Ala Leu Ser Ser Ser Pro Asn Asn Leu Ser Pro
113          290          295          300
115  aca ggc tgg tca cag ccg aaa acc ccc gtg cca gca caa aga gag cgg 1083
116  Thr Gly Trp Ser Gln Pro Lys Thr Pro Val Pro Ala Gln Arg Glu Arg
117          305          310          315
119  gca cca gta tct ggg acc cag gag aaa aac aaa att agg cct cgt gga 1131
120  Ala Pro Val Ser Gly Thr Gln Glu Lys Asn Lys Ile Arg Pro Arg Gly
121          320          325          330
123  cag aga gat tca agc tat tat tgg gaa ata gaa gcc agt gaa gtg atg 1179
124  Gln Arg Asp Ser Ser Tyr Tyr Trp Glu Ile Glu Ala Ser Glu Val Met
125          335          340          345          350
127  ctg tcc act cgg att ggg tca gcc tct ttt gga act gtt tat aag ggt 1227
128  Leu Ser Thr Arg Ile Gly Ser Gly Ser Phe Gly Thr Val Tyr Lys Gly
129          355          360          365
131  aaa tgg cac gga gat gtt gca gta aag atc cta aag gtt gtc gac cca 1275
132  Lys Trp His Gly Asp Val Ala Val Lys Ile Leu Lys Val Val Asp Pro
133          370          375          380

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135 acc cca gag caa ttc cag gcc ttc agg aat gag gtg gct gtt ctg cgc 1323
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137 385 390 395
139 aaa aca cgg cat gtg aac att ctg ctt ttc atg ggg tac atg aca aag 1371
140 Lys Thr Arg His Val Asn Ile Leu Leu Phe Met Gly Tyr Met Thr Lys
141 400 405 410
143 gac aac ctg gca att gtg acc cag tgg tgc gag ggc agc agc ctc tac 1419
144 Asp Asn Leu Ala Ile Val Thr Gln Trp Cys Glu Gly Ser Ser Leu Tyr
145 415 420 425 430
147 aaa cac ctg cat gtc cag gag acc aag ttt cag atg ttc cag cta att 1467
148 Lys His Leu His Val Gln Glu Thr Lys Phe Gln Met Phe Gln Leu Ile
149 435 440 445
151 gac att gcc cgg cag acg gct cag gga atg gac tat ttg cat gca aag 1515
152 Asp Ile Ala Arg Gln Thr Ala Gln Gly Met Asp Tyr Leu His Ala Lys
153 450 455 460
155 aac atc atc cat aga gac atg aaa tcc aac aat ata ttt ctc cat gaa 1563
156 Asn Ile Ile His Arg Asp Met Lys Ser Asn Asn Ile Phe Leu His Glu
157 465 470 475
159 ggc tta aca gtg aaa att gga gat ttt ggt ttg gca aca gta aag tca 1611
160 Gly Leu Thr Val Lys Ile Gly Asp Phe Gly Leu Ala Thr Val Lys Ser
161 480 485 490
163 cgc tgg agt ggt tct cag cag gtt gaa caa cct act ggc tct gtc ctc 1659
164 Arg Trp Ser Gly Ser Gln Gln Val Glu Gln Pro Thr Gly Ser Val Leu
165 495 500 505 510
167 tgg atg gcc cca gag gtg atc cga atg cag gat aac aac cca ttc agt 1707
168 Trp Met Ala Pro Glu Val Ile Arg Met Gln Asp Asn Asn Pro Phe Ser
169 515 520 525
171 ttc cag tgc gat gtc tac tcc tat ggc atc gta ttg tat gaa ctg atg 1755
172 Phe Gln Ser Asp Val Tyr Ser Tyr Gly Ile Val Leu Tyr Glu Leu Met
173 530 535 540
175 acg ggg gag ctt cct tat tct cac atc aac aac cga gat cag atc atc 1803
176 Thr Gly Glu Leu Pro Tyr Ser His Ile Asn Asn Arg Asp Gln Ile Ile
177 545 550 555
179 ttc atg gtg ggc cga gga tat gcc tcc cca gat ctt agt aag cta tat 1851
180 Phe Met Val Gly Arg Gly Tyr Ala Ser Pro Asp Leu Ser Lys Leu Tyr
181 560 565 570
183 aag aac tgc ccc aaa gca atg aag agg ctg gta gct gac tgt gtg aag 1899
184 Lys Asn Cys Pro Lys Ala Met Lys Arg Leu Val Ala Asp Cys Val Lys
185 575 580 585 590
187 aaa gta aag gaa gag agg cct ctt ttt ccc cag atc ctg tct tcc att 1947
188 Lys Val Lys Glu Glu Arg Pro Leu Phe Pro Gln Ile Leu Ser Ser Ile
189 595 600 605
191 gag ctg ctc caa cac tct cta ccg aag atc aac cgg agc gct tcc gag 1995
192 Glu Leu Leu Gln His Ser Leu Pro Lys Ile Asn Arg Ser Ala Ser Glu
193 610 615 620
195 cca tcc ttg cat cgg gca gcc cac act gag gat atc aat gct tgc acg 2043
196 Pro Ser Leu His Arg Ala Ala His Thr Glu Asp Ile Asn Ala Cys Thr
197 625 630 635
199 ctg acc acg tcc ccg agg ctg cct gtc ttc tagttgactt tgcacctgtc 2093

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200 Leu Thr Thr Ser Pro Arg Leu Pro Val Phe
201      640                      645
203 ttcaggctgc caggggagga ggagaagcca gcaggcacca cttttctgct ccctttctcc 2153
205 agaggcagaa cacatgtttt cagagaagct ctgctaagga ccttctagac tgctcacagg 2213
207 gccttaactt catgttgccct tcttttctat ccctttgggc cctgggagaa ggaagccatt 2273
209 tgcagtgcgt gtgtgtccctg ctccctcccc acattcccca tgctcaaggc ccagccttct 2333
211 gtagatgcgc aagtggatgt tgatggtagt acaaaaagca ggggcccagc cccagctgtt 2393
213 ggctacatga gtatttagag gaagtaaggt agcaggcagt ccagccctga tgtggagaca 2453
215 catggggtatt tggaaatcag cttctggagg aatgcattgt acaggcggga ctttcttcag 2513
217 agagtgggtgc agcggccagac attttgcaca taaggcacca aacagcccag gactgccgag 2573
219 actctggccg ccgaaggag cctgctttgg tactatggaa cttttcttag gggacacgtc 2633
221 ctcttttcac agcttctaag gtgtccagtg cattgggatg gttttccagg caaggcactc 2693
223 ggccaatccg catctcagcc ctctcaggag cagtcttcca tcatgctgaa ttttgtcttc 2753
225 caggagctgc ccctatgggg cgggcccagc ggccagcctg tttctctaac aaacaaacaa 2813
227 acaaacagcc ttgtttctct agtcacatca tgtgtataca aggaagccag gaatacaggt 2873
229 tttcttgatg atttgggttt taattttggt tttattgcac ctgacaaaat acagttatct 2933
231 gatggtccct caattatgtt attttaataa aataaattaa attt 2977
234 <210> SEQ ID NO: 2
235 <211> LENGTH: 648
236 <212> TYPE: PRT
237 <213> ORGANISM: Homo sapiens
239 <400> SEQUENCE: 2
240 Met Glu His Ile Gln Gly Ala Trp Lys Thr Ile Ser Asn Gly Phe Gly
241      1                      5                      10                      15
243 Phe Lys Asp Ala Val Phe Asp Gly Ser Ser Cys Ile Ser Pro Thr Ile
244      20                      25                      30
246 Val Gln Gln Phe Gly Tyr Gln Arg Arg Ala Ser Asp Asp Gly Lys Leu
247      35                      40                      45
249 Thr Asp Pro Ser Lys Thr Ser Asn Thr Ile Arg Val Phe Leu Pro Asn
250      50                      55                      60
252 Lys Gln Arg Thr Val Val Asn Val Arg Asn Gly Met Ser Leu His Asp
253      65                      70                      75                      80
255 Cys Leu Met Lys Ala Leu Lys Val Arg Gly Leu Gln Pro Glu Cys Cys
256      85                      90                      95
258 Ala Val Phe Arg Leu Leu His Glu His Lys Gly Lys Lys Ala Arg Leu
259      100                     105                     110
261 Asp Trp Asn Thr Asp Ala Ala Ser Leu Ile Gly Glu Glu Leu Gln Val
262      115                     120                     125
264 Asp Phe Leu Asp His Val Pro Leu Thr Thr His Asn Phe Ala Arg Lys
265      130                     135                     140
267 Thr Phe Leu Lys Leu Ala Phe Cys Asp Ile Cys Gln Lys Phe Leu Leu
268      145                     150                     155                     160
270 Asn Gly Phe Arg Cys Gln Thr Cys Gly Tyr Lys Phe His Glu His Cys
271      165                     170                     175
273 Ser Thr Lys Val Pro Thr Met Cys Val Asp Trp Ser Asn Ile Arg Gln
274      180                     185                     190
276 Leu Leu Leu Phe Pro Asn Ser Thr Ile Gly Asp Ser Gly Val Pro Ala
277      195                     200                     205
279 Leu Pro Ser Leu Thr Met Arg Arg Met Arg Glu Ser Val Ser Arg Met

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 PATENT APPLICATION: US/09/637,302

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Input Set : A:\TSR7102.txt
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280      210      215      220
282 Pro Val Ser Ser Gln His Arg Tyr Ser Thr Pro His Ala Phe Thr Phe
283 225      230      235      240
285 Asn Thr Ser Ser Pro Ser Ser Glu Gly Ser Leu Ser Gln Arg Gln Arg
286      245      250      255
288 Ser Thr Ser Thr Pro Asn Val His Met Val Ser Thr Thr Leu Pro Val
289      260      265      270
291 Asp Ser Arg Met Ile Glu Asp Ala Ile Arg Ser His Ser Glu Ser Ala
292      275      280      285
294 Ser Pro Ser Ala Leu Ser Ser Ser Pro Asn Asn Leu Ser Pro Thr Gly ..
295      290      295      300
297 Trp Ser Gln Pro Lys Thr Pro Val Pro Ala Gln Arg Glu Arg Ala Pro
298 305      310      315      320
300 Val Ser Gly Thr Gln Glu Lys Asn Lys Ile Arg Pro Arg Gly Gln Arg
301      325      330      335
303 Asp Ser Ser Tyr Tyr Trp Glu Ile Glu Ala Ser Glu Val Met Leu Ser
304      340      345      350
306 Thr Arg Ile Gly Ser Gly Ser Phe Gly Thr Val Tyr Lys Gly Lys Trp
307      355      360      365
309 His Gly Asp Val Ala Val Lys Ile Leu Lys Val Val Asp Pro Thr Pro
310      370      375      380
312 Glu Gln Phe Gln Ala Phe Arg Asn Glu Val Ala Val Leu Arg Lys Thr
313 385      390      395      400
315 Arg His Val Asn Ile Leu Leu Phe Met Gly Tyr Met Thr Lys Asp Asn
316      405      410      415
318 Leu Ala Ile Val Thr Gln Trp Cys Glu Gly Ser Ser Leu Tyr Lys His
319      420      425      430
321 Leu His Val Gln Glu Thr Lys Phe Gln Met Phe Gln Leu Ile Asp Ile
322      435      440      445
324 Ala Arg Gln Thr Ala Gln Gly Met Asp Tyr Leu His Ala Lys Asn Ile
325      450      455      460
327 Ile His Arg Asp Met Lys Ser Asn Asn Ile Phe Leu His Glu Gly Leu
328 465      470      475      480
330 Thr Val Lys Ile Gly Asp Phe Gly Leu Ala Thr Val Lys Ser Arg Trp
331      485      490      495
333 Ser Gly Ser Gln Gln Val Glu Gln Pro Thr Gly Ser Val Leu Trp Met
334      500      505      510
336 Ala Pro Glu Val Ile Arg Met Gln Asp Asn Asn Pro Phe Ser Phe Gln
337      515      520      525
339 Ser Asp Val Tyr Ser Tyr Gly Ile Val Leu Tyr Glu Leu Met Thr Gly
340      530      535      540
342 Glu Leu Pro Tyr Ser His Ile Asn Asn Arg Asp Gln Ile Ile Phe Met
343 545      550      555      560
345 Val Gly Arg Gly Tyr Ala Ser Pro Asp Leu Ser Lys Leu Tyr Lys Asn
346      565      570      575
348 Cys Pro Lys Ala Met Lys Arg Leu Val Ala Asp Cys Val Lys Lys Val
349      580      585      590
351 Lys Glu Glu Arg Pro Leu Phe Pro Gln Ile Leu Ser Ser Ile Glu Leu
352      595      600      605

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p. 6

Seq # 7

<210> 7

<211> 668

<212> PRT

<213> Artificial Sequence

<400> 7

Met Glu His Ile Gln Gly Ala Trp Lys Thr Ile Ser Asn Gly Phe Gly
1 5 10 15

missing mandatory <220> and <223> features to
explain artificial sequence. See #12 on
Error Summary Sheet. * Also see #7 on

Error Summary Sheet

VERIFICATION SUMMARY DATE: 08/23/2000
PATENT APPLICATION: US/09/637,302 TIME: 09:32:55

Input Set : A:\TSR7102.txt
Output Set: N:\CRF3\08232000\I637302.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:892 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:892 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: